

## SEQUENCE LISTING

- <110> FUKUCHI, Naoyuki  
FUTAKI, Fumie  
KITO, Morikazu  
SATO, Seiichi  
KAJIURA, Takayuki  
ONO, Yukitsugu  
TANAKA, Akiko  
SHINOZAKI, Junko
- <120> Substance with Antithrombic Activity and  
Method for Detecting Glycocalicin
- <130> OP818-PCT
- <140> PCT/JP99/00089
- <141> 1998-01-13
- <150> JP 10-113962
- <151> 1998-04-23
- <160> 14
- <170> PatentIn Ver. 2.0
- <210> 1
- <211> 36
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:primer
- <400> 1  
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- <210> 2
- <211> 29
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Description of Artificial Sequence:primer

&lt;400&gt; 2

atatctagat gtgcccaggg attgtggtt

29

&lt;210&gt; 3

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;400&gt; 3

ataaagcttc tcgagtcatt taccaggaga gtggga

36

&lt;210&gt; 4

&lt;211&gt; 684

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(684)

&lt;400&gt; 4

gtg ccc agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa	48
Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu	
1 5 10 15	
gta tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc	96
Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr	
20 25 30	
att act ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag	144
Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys	
35 40 45	
gat gat ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg	192
Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val	
50 55 60	
cac aca gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc	240
His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe	
65 70 75 80	
cgc tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc	288
Arg Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly	
85 90 95	
aag gag ttc aaa tgc agg gta aac agt gca gct ttc cct gcc ccc atc	336

Lys	Glu	Phe	Lys	Cys	Arg	Val	Asn	Ser	Ala	Ala	Phe	Pro	Ala	Pro	Ile		
			100					105					110				
gag	aaa	acc	atc	tcc	aaa	acc	aaa	ggc	aga	ccg	aag	gct	cca	cag	gtg	384	
Glu	Lys	Thr	Ile	Ser	Lys	Thr	Lys	Gly	Arg	Pro	Lys	Ala	Pro	Gln	Val		
		115					120					125					
tac	acc	att	cca	cct	ccc	aag	gag	cag	atg	gcc	aag	gat	aaa	gtc	agt	432	
Tyr	Thr	Ile	Pro	Pro	Pro	Lys	Glu	Gln	Met	Ala	Lys	Asp	Lys	Val	Ser		
		130				135					140						
ctg	acc	tgc	atg	ata	aca	gac	ttc	ttc	cct	gaa	gac	att	act	gtg	gag	480	
Leu	Thr	Cys	Met	Ile	Thr	Asp	Phe	Phe	Pro	Glu	Asp	Ile	Thr	Val	Glu		
145					150				155				160				
tgg	cag	tgg	aat	ggg	cag	cca	gcg	gag	aac	tac	aag	aac	act	cag	ccc	528	
Trp	Gln	Trp	Asn	Gly	Gln	Pro	Ala	Glu	Asn	Tyr	Lys	Asn	Thr	Gln	Pro		
			165					170					175				
atc	atg	gac	aca	gat	ggc	tct	tac	ttc	gtc	tac	agc	aag	ctc	aat	gtg	576	
Ile	Met	Asp	Thr	Asp	Gly	Ser	Tyr	Phe	Val	Tyr	Ser	Lys	Leu	Asn	Val		
		180					185					190					
cag	aag	agc	aac	tgg	gag	gca	gga	aat	act	ttc	acc	tgc	tct	gtg	tta	624	
Gln	Lys	Ser	Asn	Trp	Glu	Ala	Gly	Asn	Thr	Phe	Thr	Cys	Ser	Val	Leu		
		195				200						205					
cat	gag	ggc	ctg	cac	aac	cac	cat	act	gag	aag	agc	ctc	tcc	cac	tct	672	
His	Glu	Gly	Leu	His	Asn	His	His	Thr	Glu	Lys	Ser	Leu	Ser	His	Ser		
	210				215				220								
cct	ggt	aaa	tga													684	
Pro	Gly	Lys															
225																	

&lt;210&gt; 5

&lt;211&gt; 227

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 5

Val	Pro	Arg	Asp	Cys	Gly	Cys	Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu		
1				5				10					15				
Val	Ser	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr		
			20				25					30					
Ile	Thr	Leu	Thr	Pro	Lys	Val	Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys		
		35				40						45					
Asp	Asp	Pro	Glu	Val	Gln	Phe	Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val		
	50				55				60								
His	Thr	Ala	Gln	Thr	Gln	Pro	Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Phe		
65					70				75						80		

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<210> 6

<211> 1689

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of  
genes of *Mus musculus* and *Homo sapiens*

$\langle 220 \rangle$

<221> CDS

<222> (1)..(1689)

<220>

<221> sig\_peptide

<222> (1)..(48)

$\langle 220 \rangle$

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<221> mat_peptide
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<222> (49)..(1689)

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Met Pro Leu Leu Leu Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro	
-16 -15 -10 -5	
cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac	96
His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn	
1 5 10 15	
tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac	144
Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp	
20 25 30	
aca acc atc ctc cac ctg agt gag aac ctc ctg tac acc ttc tcc ctg	192
Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu	
35 40 45	
gca acc ctg atg cct tac act cgc ctc act cag ctg aac cta gat agg	240
Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg	
50 55 60	
tgc gag ctc acc aag ctc cag gtc gat ggg acg ctg cca gtg ctg ggg	288
Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly	
65 70 75 80	
acc ctg gat cta tcc cac aat cag ctg caa agc ctg ccc ttg cta ggg	336
Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly	
85 90 95	
cag aca ctg cct gct ctc acc gtc ctg gac gtc tcc ttc aac cgg ctg	384
Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu	
100 105 110	
acc tcg ctg cct ctt ggt gcc ctg cgt ggt ctt ggc gaa ctc caa gag	432
Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu	
115 120 125	
ctc tac ctg aaa ggc aat gag ctg aag acc ctg ccc cca ggg ctc ctg	480
Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu	
130 135 140	
acg ccc aca ccc aag ctg gag aag ctc agt ctg gct aac aac aac ttg	528
Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu	
145 150 155 160	
act gag ctc ccc gct ggg ctc ctg aat ggg ctg gag aat ctc gac acc	576
Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr	
165 170 175	
ctt ctc ctc caa gag aac tcg ctg tat aca ata cca aag ggc ttt ttt	624
Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe	
180 185 190	
ggg tcc cac ctc ctg cct ttt gct ttt ctc cac ggg aac ccc tgg tta	672
Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu	
195 200 205	
tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct	720

Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala	
210 215 220	
gaa aat gtc tac gta tgg aag caa ggt gtg gac gtc aag gcc atg acc	768
Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr	
225 230 235 240	
tct aac gtg gcc agt gtg cag tgt gac aat tca gac aag ttt ccc gtc	816
Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val	
245 250 255	
tac aaa tac cca gga aag ggg tgc ccc acc ctt ggt gat gaa ggt gac	864
Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp	
260 265 270	
aca gac cta tat gat tac tac cca gaa gag gac act gag ggc gat aag	912
Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys	
275 280 285	
gtg cgt gcc aca agg act gtg gtc aag ttc ccc acc aaa gcc cat aca	960
Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr	
290 295 300	
acc ccc tgg ggt cta ttc tac tca tgg tcc act gct tct cta gac gtg	1008
Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Val	
305 310 315 320	
ccc agg gat tgt ggt tgt aag cct tgc ata tgt aca gtc cca gaa gta	1056
Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val	
325 330 335	
tca tct gtc ttc atc ttc ccc cca aag ccc aag gat gtg ctc acc att	1104
Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile	
340 345 350	
act ctg act cct aag gtc acg tgt gtt gtg gta gac atc agc aag gat	1152
Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp	
355 360 365	
gat ccc gag gtc cag ttc agc tgg ttt gta gat gat gtg gag gtg cac	1200
Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His	
370 375 380	
aca gct cag acg caa ccc cgg gag gag cag ttc aac agc act ttc cgc	1248
Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg	
385 390 395 400	
tca gtc agt gaa ctt ccc atc atg cac cag gac tgg ctc aat ggc aag	1296
Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys	
405 410 415	
gag ttc aaa tgc agg gta aac agt gca gct ttc cct gcc ccc atc gag	1344
Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu	
420 425 430	
aaa acc atc tcc aaa acc aaa ggc aga ccg aag gct cca cag gtg tac	1392
Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr	

435	440	445	
acc att cca cct ccc aag gag cag atg gcc aag gat aaa gtc agt ctg			1440
Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu			
450	455	460	
acc tgc atg ata aca gac ttc ttc cct gaa gac att act gtg gag tgg			1488
Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp			
465	470	475	480
cag tgg aat ggg cag cca gcg gag aac tac aag aac act cag ccc atc			1536
Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile			
485	490	495	
atg gac aca gat ggc tct tac ttc gtc tac agc aag ctc aat gtg cag			1584
Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln			
500	505	510	
aag agc aac tgg gag gca gga aat act ttc acc tgc tct gtg tta cat			1632
Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His			
515	520	525	
gag ggc ctg cac aac cac cat act gag aag agc ctc tcc cac tct cct			1680
Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro			
530	535	540	
ggt aaa tga			1689
Gly Lys			
545			

&lt;210&gt; 7

&lt;211&gt; 562

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:chimera of  
genes of Mus musculus and Homo sapiens

&lt;400&gt; 7

Met Pro Leu Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro	
-16 -15	-10 -5
His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn	
1 5 10 15	
Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp	
20 25 30	
Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu	
35 40 45	
Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg	
50 55 60	

Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly  
 65 70 75 80  
 Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly  
 85 90 95  
 Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu  
 100 105 110  
 Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu  
 115 120 125  
 Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu  
 130 135 140  
 Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu  
 145 150 155 160  
 Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr  
 165 170 175  
 Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe  
 180 185 190  
 Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu  
 195 200 205  
 Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala  
 210 215 220  
 Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr  
 225 230 235 240  
 Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val  
 245 250 255  
 Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp  
 260 265 270  
 Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys  
 275 280 285  
 Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr  
 290 295 300  
 Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Val  
 305 310 315 320  
 Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile Cys Thr Val Pro Glu Val  
 325 330 335  
 Ser Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Val Leu Thr Ile  
 340 345 350  
 Thr Leu Thr Pro Lys Val Thr Cys Val Val Val Asp Ile Ser Lys Asp  
 355 360 365  
 Asp Pro Glu Val Gln Phe Ser Trp Phe Val Asp Asp Val Glu Val His  
 370 375 380  
 Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg  
 385 390 395 400  
 Ser Val Ser Glu Leu Pro Ile Met His Gln Asp Trp Leu Asn Gly Lys



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405 410 415  
Glu Phe Lys Cys Arg Val Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu  
420 425 430  
Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr  
435 440 445  
Thr Ile Pro Pro Pro Lys Glu Gln Met Ala Lys Asp Lys Val Ser Leu  
450 455 460  
Thr Cys Met Ile Thr Asp Phe Phe Pro Glu Asp Ile Thr Val Glu Trp  
465 470 475 480  
Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile  
485 490 495  
Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln  
500 505 510  
Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe Thr Cys Ser Val Leu His  
515 520 525  
Glu Gly Leu His Asn His His Thr Glu Lys Ser Leu Ser His Ser Pro  
530 535 540  
Gly Lys  
545

<210> 8  
<211> 30  
<212> DNA  
<213> Artificial Sequence

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<223> Description of Artificial Sequence:primer

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30

<210> 9  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

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44

<210> 10

<211> 729  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:chimera of genes of Mus musculus and Homo sapiens

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 <221> CDS  
 <222> (7)..(708)

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           1                  5                  10  
 tgc cca gca cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct 96  
 Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro  
   15                  20                  25                  30  
 cca aag atc aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca 144  
 Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr  
                   35                  40                  45  
 tgt gtg gtg gtg gat gtg agc gag gat gac cca gat gtc cag atc agc 192  
 Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser  
                   50                  55                  60  
 tgg ttt gtg aac aac gtg gaa gta cac aca gct cag aca caa acc cat 240  
 Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His  
                   65                  70                  75  
 aga gag gat tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc 288  
 Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile  
                   80                  85                  90  
 cag cac cag gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac 336  
 Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn  
   95                  100                  105                  110  
 aac aaa gac ctg cca gcg ccc atc gag aga acc atc tca aaa ccc aaa 384  
 Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys  
                   115                  120                  125  
 ggg tca gta aga gct cca cag gta tat gtc ttg cct cca cca gaa gaa 432  
 Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu  
                   130                  135                  140  
 gag atg act aag aaa cag gtc act ctg acc tgc atg gtc aca gac ttc 480  
 Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe  
                   145                  150                  155  
 atg cct gaa gac att tac gtg gag tgg acc aac aac ggg aaa aca gag 528

Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu  
 160 165 170  
 cta aac tac aag aac act gaa cca gtc ctg gac tct gat ggt tct tac 576  
 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr  
 175 180 185 190  
 ttc atg tac agc aag ctg aga gtg gaa aag aag aac tgg gtg gaa aga 624  
 Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg  
 195 200 205  
 aat agc tac tcc tgt tca gtg gtc cac gag ggt ctg cac aat cac cac 672  
 Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His  
 210 215 220  
 acg act aag agc ttc tcc cgg act ccg ggt aaa tgaaaggatat gtctcgagaa 725  
 Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys  
 225 230  
 gctt 729

&lt;210&gt; 11

&lt;211&gt; 233

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:chimera of  
genes of Mus musculus and Homo sapiens

&lt;400&gt; 11

Glu Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro  
 1 5 10 15  
 Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys  
 20 25 30  
 Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val  
 35 40 45  
 Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe  
 50 55 60  
 Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu  
 65 70 75 80  
 Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His  
 85 90 95  
 Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys  
 100 105 110  
 Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser  
 115 120 125  
 Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met

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130		135		140											
Thr	Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro
145					150					155					160
Glu	Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn
				165					170						175
Tyr	Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met
			180					185					190		
Tyr	Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser
		195					200					205			
Tyr	Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr
	210					215					220				
Lys	Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys							
225					230										

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

agctatctag acgagcccag agggcccaca

30

<210> 13

<211> 1707

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:chimera of  
genes of Mus musculus and Homo sapiens

<220>

<221> CDS

<222> (1)..(1707)

<220>

<221> sig\_peptide

<222> (1)..(48)

<220>

&lt;221&gt; mat\_peptide

&lt;222&gt; (49)..(1704)

&lt;400&gt; 13

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atg cct ctc ctc ctc ttg ctg ctc ctg ctg cca agc ccc tta cac ccc 48
Met Pro Leu Leu Leu Leu Leu Leu Leu Leu Pro Ser Pro Leu His Pro
-16 -15 -10 -5
cac ccc atc tgt gag gtc tcc aaa gtg gcc agc cac cta gaa gtg aac 96
His Pro Ile Cys Glu Val Ser Lys Val Ala Ser His Leu Glu Val Asn
1 5 10 15
tgt gac aag agg aat ctg aca gcg ctg cct cca gac ctg ccg aaa gac 144
Cys Asp Lys Arg Asn Leu Thr Ala Leu Pro Pro Asp Leu Pro Lys Asp
20 25 30
aca acc atc ctc cac ctg agt gag aac ctc ctg tac acc ttc tcc ctg 192
Thr Thr Ile Leu His Leu Ser Glu Asn Leu Leu Tyr Thr Phe Ser Leu
35 40 45
gca acc ctg atg cct tac act cgc ctc act cag ctg aac cta gat agg 240
Ala Thr Leu Met Pro Tyr Thr Arg Leu Thr Gln Leu Asn Leu Asp Arg
50 55 60
tgc gag ctc acc aag ctc cag gtc gat ggg acg ctg cca gtg ctg ggg 288
Cys Glu Leu Thr Lys Leu Gln Val Asp Gly Thr Leu Pro Val Leu Gly
65 70 75 80
acc ctg gat cta tcc cac aat cag ctg caa agc ctg ccc ttg cta ggg 336
Thr Leu Asp Leu Ser His Asn Gln Leu Gln Ser Leu Pro Leu Leu Gly
85 90 95
cag aca ctg cct gct ctc acc gtc ctg gac gtc tcc ttc aac cgg ctg 384
Gln Thr Leu Pro Ala Leu Thr Val Leu Asp Val Ser Phe Asn Arg Leu
100 105 110
acc tcg ctg cct ctt ggt gcc ctg cgt ggt ctt ggc gaa ctc caa gag 432
Thr Ser Leu Pro Leu Gly Ala Leu Arg Gly Leu Gly Glu Leu Gln Glu
115 120 125
ctc tac ctg aaa ggc aat gag ctg aag acc ctg ccc cca ggg ctc ctg 480
Leu Tyr Leu Lys Gly Asn Glu Leu Lys Thr Leu Pro Pro Gly Leu Leu
130 135 140
acg ccc aca ccc aag ctg gag aag ctc agt ctg gct aac aac aac ttg 528
Thr Pro Thr Pro Lys Leu Glu Lys Leu Ser Leu Ala Asn Asn Asn Leu
145 150 155 160
act gag ctc ccc gct ggg ctc ctg aat ggg ctg gag aat ctc gac acc 576
Thr Glu Leu Pro Ala Gly Leu Leu Asn Gly Leu Glu Asn Leu Asp Thr
165 170 175
ctt ctc ctc caa gag aac tcg ctg tat aca ata cca aag ggc ttt ttt 624
Leu Leu Leu Gln Glu Asn Ser Leu Tyr Thr Ile Pro Lys Gly Phe Phe
180 185 190

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ggg tcc cac ctc ctg cct ttt gct ttt ctc cac ggg aac ccc tgg tta	672
Gly Ser His Leu Leu Pro Phe Ala Phe Leu His Gly Asn Pro Trp Leu	
195 200 205	
tgc aac tgt gag atc ctc tat ttt cgt cgc tgg ctg cag gac aat gct	720
Cys Asn Cys Glu Ile Leu Tyr Phe Arg Arg Trp Leu Gln Asp Asn Ala	
210 215 220	
gaa aat gtc tac gta tgg aag caa ggt gtg gac gtc aag gcc atg acc	768
Glu Asn Val Tyr Val Trp Lys Gln Gly Val Asp Val Lys Ala Met Thr	
225 230 235 240	
tct aac gtg gcc agt gtg cag tgt gac aat tca gac aag ttt ccc gtc	816
Ser Asn Val Ala Ser Val Gln Cys Asp Asn Ser Asp Lys Phe Pro Val	
245 250 255	
tac aaa tac cca gga aag ggg tgc ccc acc ctt ggt gat gaa ggt gac	864
Tyr Lys Tyr Pro Gly Lys Gly Cys Pro Thr Leu Gly Asp Glu Gly Asp	
260 265 270	
aca gac cta tat gat tac tac cca gaa gag gac act gag ggc gat aag	912
Thr Asp Leu Tyr Asp Tyr Tyr Pro Glu Glu Asp Thr Glu Gly Asp Lys	
275 280 285	
gtg cgt gcc aca agg act gtg gtc aag ttc ccc acc aaa gcc cat aca	960
Val Arg Ala Thr Arg Thr Val Val Lys Phe Pro Thr Lys Ala His Thr	
290 295 300	
acc ccc tgg ggt cta ttc tac tca tgg tcc act gct tct cta gac gag	1008
Thr Pro Trp Gly Leu Phe Tyr Ser Trp Ser Thr Ala Ser Leu Asp Glu	
305 310 315 320	
ccc aga ggg ccc aca atc aag ccc tgt cct cca tgc aaa tgc cca gca	1056
Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala	
325 330 335	
cct aac ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag atc	1104
Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile	
340 345 350	
aag gat gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg	1152
Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val	
355 360 365	
gtg gat gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt gtg	1200
Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val	
370 375 380	
aac aac gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat	1248
Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp	
385 390 395 400	
tac aac agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag	1296
Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln	
405 410 415	
gac tgg atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac	1344

Asp	Trp	Met	Ser	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Asp	
			420					425					430			
ctg	cca	gcg	ccc	atc	gag	aga	acc	atc	tca	aaa	ccc	aaa	ggg	tca	gta	1392
Leu	Pro	Ala	Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Pro	Lys	Gly	Ser	Val	
			435					440					445			
aga	gct	cca	cag	gta	tat	gtc	ttg	cct	cca	cca	gaa	gaa	gag	atg	act	1440
Arg	Ala	Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	
			450					455					460			
aag	aaa	cag	gtc	act	ctg	acc	tgc	atg	gtc	aca	gac	ttc	atg	cct	gaa	1488
Lys	Lys	Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	
			465				470				475				480	
gac	att	tac	gtg	gag	tgg	acc	aac	aac	ggg	aaa	aca	gag	cta	aac	tac	1536
Asp	Ile	Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	
			485						490					495		
aag	aac	act	gaa	cca	gtc	ctg	gac	tct	gat	ggt	tct	tac	ttc	atg	tac	1584
Lys	Asn	Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	
			500					505					510			
agc	aag	ctg	aga	gtg	gaa	aag	aag	aac	tgg	gtg	gaa	aga	aat	agc	tac	1632
Ser	Lys	Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	
			515					520					525			
tcc	tgt	tca	gtg	gtc	cac	gag	ggt	ctg	cac	aat	cac	cac	acg	act	aag	1680
Ser	Cys	Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	
			530				535					540				
agc	ttc	tcc	cgg	act	ccg	ggt	aaa	tga								1707
Ser	Phe	Ser	Arg	Thr	Pro	Gly	Lys									
			545				550									

&lt;210&gt; 14

&lt;211&gt; 568

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:chimera of  
genes of Mus musculus and Homo sapiens

&lt;400&gt; 14

Met	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Ser	Pro	Leu	His	Pro	
-16	-15					-10				-5					
His	Pro	Ile	Cys	Glu	Val	Ser	Lys	Val	Ala	Ser	His	Leu	Glu	Val	Asn
1				5					10				15		
Cys	Asp	Lys	Arg	Asn	Leu	Thr	Ala	Leu	Pro	Pro	Asp	Leu	Pro	Lys	Asp
			20					25					30		

Thr	Thr	Ile	Leu	His	Leu	Ser	Glu	Asn	Leu	Leu	Tyr	Thr	Phe	Ser	Leu	35	40	45
Ala	Thr	Leu	Met	Pro	Tyr	Thr	Arg	Leu	Thr	Gln	Leu	Asn	Leu	Asp	Arg	50	55	60
Cys	Glu	Leu	Thr	Lys	Leu	Gln	Val	Asp	Gly	Thr	Leu	Pro	Val	Leu	Gly	65	70	75
Thr	Leu	Asp	Leu	Ser	His	Asn	Gln	Leu	Gln	Ser	Leu	Pro	Leu	Leu	Gly	85	90	95
Gln	Thr	Leu	Pro	Ala	Leu	Thr	Val	Leu	Asp	Val	Ser	Phe	Asn	Arg	Leu	100	105	110
Thr	Ser	Leu	Pro	Leu	Gly	Ala	Leu	Arg	Gly	Leu	Gly	Glu	Leu	Gln	Glu	115	120	125
Leu	Tyr	Leu	Lys	Gly	Asn	Glu	Leu	Lys	Thr	Leu	Pro	Pro	Gly	Leu	Leu	130	135	140
Thr	Pro	Thr	Pro	Lys	Leu	Glu	Lys	Leu	Ser	Leu	Ala	Asn	Asn	Asn	Leu	145	150	155
Thr	Glu	Leu	Pro	Ala	Gly	Leu	Leu	Asn	Gly	Leu	Glu	Asn	Leu	Asp	Thr	165	170	175
Leu	Leu	Leu	Gln	Glu	Asn	Ser	Leu	Tyr	Thr	Ile	Pro	Lys	Gly	Phe	Phe	180	185	190
Gly	Ser	His	Leu	Leu	Pro	Phe	Ala	Phe	Leu	His	Gly	Asn	Pro	Trp	Leu	195	200	205
Cys	Asn	Cys	Glu	Ile	Leu	Tyr	Phe	Arg	Arg	Trp	Leu	Gln	Asp	Asn	Ala	210	215	220
Glu	Asn	Val	Tyr	Val	Trp	Lys	Gln	Gly	Val	Asp	Val	Lys	Ala	Met	Thr	225	230	235
Ser	Asn	Val	Ala	Ser	Val	Gln	Cys	Asp	Asn	Ser	Asp	Lys	Phe	Pro	Val	245	250	255
Tyr	Lys	Tyr	Pro	Gly	Lys	Gly	Cys	Pro	Thr	Leu	Gly	Asp	Glu	Gly	Asp	260	265	270
Thr	Asp	Leu	Tyr	Asp	Tyr	Tyr	Pro	Glu	Glu	Asp	Thr	Glu	Gly	Asp	Lys	275	280	285
Val	Arg	Ala	Thr	Arg	Thr	Val	Val	Lys	Phe	Pro	Thr	Lys	Ala	His	Thr	290	295	300
Thr	Pro	Trp	Gly	Leu	Phe	Tyr	Ser	Trp	Ser	Thr	Ala	Ser	Leu	Asp	Glu	305	310	315
Pro	Arg	Gly	Pro	Thr	Ile	Lys	Pro	Cys	Pro	Pro	Cys	Lys	Cys	Pro	Ala	325	330	335
Pro	Asn	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Ile	340	345	350
Lys	Asp	Val	Leu	Met	Ile	Ser	Leu	Ser	Pro	Ile	Val	Thr	Cys	Val	Val	355	360	365
Val	Asp	Val	Ser	Glu	Asp	Asp	Pro	Asp	Val	Gln	Ile	Ser	Trp	Phe	Val			



370	375	380
Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp		
385	390	395
Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln		400
	405	410
Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp		415
	420	425
Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val		430
	435	440
Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr		445
	450	455
Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu		460
465	470	475
Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr		480
	485	490
Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr		495
	500	505
Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr		510
	515	520
Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys		525
	530	535
Ser Phe Ser Arg Thr Pro Gly Lys		540
545	550	